

SCORE Search Results Details for Application 10522366 and Search Result 20071205_094818_us-10-522-366a- 18.p2n.rnpbm.

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OM protein - nucleic search, using frame_plus_p2n model

Run on: December 5, 2007, 09:54:43 ; Search time 2755 Seconds
(without alignments)
947.414 Million cell updates/sec

Title: US-10-522-366A-18

Perfect score: 620

Sequence: 1 AENNLNDEKNKPRKGFKDYG.....PKTGNQLKGPDPKRNIKKYL 110

Scoring table: BLOSUM62

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Ygapop	10.0	Ygapext	0.5
Fgapop	6.0	Fgapext	7.0
Delop	6.0	Delext	7.0

Searched: 31364175 seqs, 11865555624 residues

Total number of hits satisfying chosen parameters: 62727632

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-NORM=ext -HEAPSIZE=0 -MINLEN=0 -MAXLEN=2000000000 -MINDBSEQLEN=1 -HOST=ai6-01
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query				Description
			Match	Length	DB	ID	
	1	620	100.0	5537	18	US-11-010-599-21	Sequence 21, Appl
	2	620	100.0	5572	18	US-11-010-599-7	Sequence 7, Appl
	3	620	100.0	7117	10	US-10-738-423-34	Sequence 34, Appl
	4	620	100.0	7117	20	US-11-082-544-34	Sequence 34, Appl
c	5	98.5	15.9	1541	26	US-11-443-428A-494070	Sequence 494070,
	6	97.5	15.7	560	9	US-10-424-599-52483	Sequence 52483, A
	7	94.5	15.2	429	9	US-10-021-323-3040	Sequence 3040, Ap
	8	94.5	15.2	429	22	US-11-292-078-3040	Sequence 3040, Ap
	9	94	15.2	575	10	US-10-425-115-46819	Sequence 46819, A
c	10	92	14.8	366	11	US-10-501-282-4441	Sequence 4441, Ap
	11	92	14.8	1029	13	US-10-953-349-30803	Sequence 30803, A
	12	92	14.8	2373	11	US-10-501-282-4435	Sequence 4435, Ap
c	13	92	14.8	4383	16	US-10-777-288A-649	Sequence 649, App
	14	92	14.8	8022	6	US-09-815-264-66785	Sequence 66785, A
	15	92	14.8	8022	23	US-11-491-125A-65966	Sequence 65966, A
	16	92	14.8	8022	27	US-11-595-983-66785	Sequence 66785, A
c	17	92	14.8	1754382	11	US-10-501-282-6651	Sequence 6651, Ap
c	18	91.5	14.8	607	13	US-10-301-480-598866	Sequence 598866,
c	19	91.5	14.8	607	13	US-10-301-480-1212275	Sequence 1212275,
c	20	91.5	14.8	40325	23	US-11-033-545-580	Sequence 580, App
c	21	91.5	14.8	40325	23	US-11-033-545-771	Sequence 771, App
c	22	91.5	14.8	48287	16	US-10-990-328-97872	Sequence 97872, A

c	23	91	14.7	581	9	US-10-424-599-25276	Sequence 25276, A
	24	91	14.7	2795	9	US-10-676-248B-54	Sequence 54, Appl
	25	91	14.7	35964	22	US-11-177-646-580	Sequence 580, App
	26	91	14.7	35965	22	US-11-177-646-579	Sequence 579, App
	27	90.5	14.6	488	9	US-10-021-323-2155	Sequence 2155, Ap
	28	90.5	14.6	488	22	US-11-292-078-2155	Sequence 2155, Ap
	29	90.5	14.6	881	26	US-11-443-428A-499375	Sequence 499375,
c	30	90	14.5	3610	23	US-11-491-125A-1457	Sequence 1457, Ap
	31	89.5	14.4	443	9	US-10-424-599-138614	Sequence 138614,
c	32	89.5	14.4	601	16	US-10-940-774-131726	Sequence 131726,
	33	89.5	14.4	796	7	US-10-027-632-142081	Sequence 142081,
	34	89.5	14.4	796	7	US-10-027-632-142083	Sequence 142083,
	35	89.5	14.4	796	8	US-10-027-632-142081	Sequence 142081,
	36	89.5	14.4	796	8	US-10-027-632-142083	Sequence 142083,
	37	89.5	14.4	6333	16	US-10-940-774-15447	Sequence 15447, A
	38	89.5	14.4	16684	16	US-10-990-328-94837	Sequence 94837, A
	39	89	14.4	14257	6	US-09-815-264-64955	Sequence 64955, A
	40	89	14.4	14257	23	US-11-491-125A-38644	Sequence 38644, A
	41	89	14.4	14257	27	US-11-595-983-64955	Sequence 64955, A
	42	89	14.4	36614	6	US-09-815-264-65666	Sequence 65666, A
	43	89	14.4	36614	27	US-11-595-983-65666	Sequence 65666, A
	44	88.5	14.3	491	10	US-10-425-115-171055	Sequence 171055,
	45	88.5	14.3	594	9	US-10-021-323-15774	Sequence 15774, A

ALIGNMENTS

RESULT 1

US-11-010-599-21

; Sequence 21, Application US/11010599
 ; Publication No. US20050181395A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anthony, Larry
 ; APPLICANT: Filutowicz, Marcin
 ; APPLICANT: Suzuki, Hideki
 ; TITLE OF INVENTION: Systems for Tightly Regulated Gene Expression
 ; FILE REFERENCE: CONJUGON-09431
 ; CURRENT APPLICATION NUMBER: US/11/010,599
 ; CURRENT FILING DATE: 2004-12-13
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 21
 ; LENGTH: 5537
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic

US-11-010-599-21

Alignment Scores:

Pred. No.:	2.28e-65	Length:	5537
Score:	620.00	Matches:	110
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
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DB:	18	Gaps:	0

US-10-522-366A-18 (1-110) x US-11-010-599-21 (1-5537)

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Db 1748 GCTGAAAATAATTAAACGATGAAAAGAATAAGCCCAGAAAGGTTTAAAGATTACGGG 1807
 Qy 21 HisAspTyrHisProAlaProLysThrGluAsnIleLysGlyLeuGlyAspLeuLysPro 40
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 Db 1808 CATGATTATCATCCAGCTCCGAAAAGTGAGAATATTAAAGGCTTGGTGTCTTAAGCCT 1867
 Qy 41 GlyIleProLysThrProLysGlnAsnGlyGlyLysArgLysArgTrpThrGlyAsp 60
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 Db 1868 GGGATACCAAAAAACACCAAAGCAGAATGGTGGTGGAAAACGCAAGCGCTGGACTGGAGAT 1927
 Qy 61 LysGlyArgLysIleTyrGluTrpAspSerGlnHisGlyGluLeuGluGlyTyrArgAla 80
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 Db 1928 AAAGGGCGTAAGATTATGAGTGGGATTCTCAGCATGGTGAGCTTGAGGGGTATCGTGCC 1987
 Qy 81 SerAspGlyGlnHisLeuGlySerPheAspProLysThrGlyAsnGlnLeuLysGlyPro 100
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 Db 1988 AGTGATGGTCAGCATCTGGCTCATTGACCTAAACAGGCAATCAGTTGAAAGGTCCA 2047
 Qy 101 AspProLysArgAsnIleLysLysTyrLeu 110
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 Db 2048 GATCCGAAACGAAATATCAAGAAATATCTT 2077

RESULT 2

US-11-010-599-7

; Sequence 7, Application US/11010599
 ; Publication No. US20050181395A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anthony, Larry
 ; APPLICANT: Filutowicz, Marcin
 ; APPLICANT: Suzuki, Hideki
 ; TITLE OF INVENTION: Systems for Tightly Regulated Gene Expression
 ; FILE REFERENCE: CONJUGON-09431
 ; CURRENT APPLICATION NUMBER: US/11/010,599
 ; CURRENT FILING DATE: 2004-12-13
 ; NUMBER OF SEQ ID NOS: 21
 ; SOFTWARE: PatentIn version 3.3
 ; SEQ ID NO 7
 ; LENGTH: 5572
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Synthetic

US-11-010-599-7

Alignment Scores:

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Score:	620.00	Matches:	110
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Query Match:	100.0%	Indels:	0
DB:	18	Gaps:	0

US-10-522-366A-18 (1-110) x US-11-010-599-7 (1-5572)

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 Qy 21 HisAspTyrHisProAlaProLysThrGluAsnIleLysGlyLeuGlyAspLeuLysPro 40
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 Db 1399 CATGATTATCATCCAGCTCCGAAAAGTGAGAATATTAAAGGCTTGGTGTCTTAAGCCT 1458

Qy 41 GlyIleProLysThrProLysGlnAsnGlyGlyGlyLysArgLysArgTrpThrGlyAsp 60
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Qy 61 LysGlyArgLysIleTyrGluTrpAspSerGlnHisGlyGluLeuGluGlyTyrArgAla 80
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Qy 81 SerAspGlyGlnHisLeuGlySerPheAspProLysThrGlyAsnGlnLeuLysGlyPro 100
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Db 1579 AGTGATGGTCAGCATCTGGCTCATTGACCCTAAAACAGGCAATCAGTTGAAAGGTCCA 1638

Qy 101 AspProLysArgAsnIleLysLysTyrLeu 110
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Db 1639 GATCCGAAACGAAATATCAAGAAATATCTT 1668

<!--StartFragment-->RESULT 3
 US-10-738-423-34
 ; Sequence 34, Application US/10738423
 ; Publication No. US20040229338A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Bermudes, G.
 ; APPLICANT: King, I.
 ; APPLICANT: Clairmont, C.
 ; APPLICANT: Lin, S.
 ; APPLICANT: Belcourt, M.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR
 ; TITLE OF INVENTION: TUMOR-TARGETED DELIVERY OF EFFECTOR MOLECULES
 ; FILE REFERENCE: 8002-059
 ; CURRENT APPLICATION NUMBER: US/10/738,423
 ; CURRENT FILING DATE: 2003-12-16
 ; PRIOR APPLICATION NUMBER: US/09/645,415
 ; PRIOR FILING DATE: 2000-08-24
 ; PRIOR APPLICATION NUMBER: 60/157,581
 ; PRIOR FILING DATE: 1999-10-04
 ; PRIOR APPLICATION NUMBER: 60/157,637
 ; PRIOR FILING DATE: 1999-10-04
 ; NUMBER OF SEQ ID NOS: 61
 ; SOFTWARE: FastSEQ for Windows Version 3.0
 ; SEQ ID NO 34
 ; LENGTH: 7117
 ; TYPE: DNA
 ; ORGANISM: E. coli
 US-10-738-423-34

Alignment Scores:

Pred. No.:	3.04e-65	Length:	7117
Score:	620.00	Matches:	110
Percent Similarity:	100.0%	Conservative:	0
Best Local Similarity:	100.0%	Mismatches:	0
Query Match:	100.0%	Indels:	0
DB:	10	Gaps:	0

US-10-522-366A-18 (1-110) x US-10-738-423-34 (1-7117)

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Qy	21 HisAspTyrHisProAlaProLysThrGluAsnIleLysGlyLeuGlyAspLeuLysPro 40
Db	1646 CATGATTATCATCAGCTCCGAAACTGAGAATATTAAAGGCTTGGTATCTTAAGCCT 1705
Qy	41 GlyIleProLysThrProLysGlnAsnGlyGlyLysArgLysArgTrpThrGlyAsp 60
Db	1706 GGGATACCAAAACACCAAAGCAGAATGGTGGTGGAAAACGCAAGCGCTGGACTGGAGAT 1765
Qy	61 LysGlyArgLysIleTyrGluTrpAspSerGlnHisGlyGluLeuGluGlyTyrArgAla 80
Db	1766 AAAGGGCGTAAGATTATGAGTGGATTCTCAGCATGGTGAGCTTGAGGGGTATCGTGCC 1825
Qy	81 SerAspGlyGlnHisLeuGlySerPheAspProLysThrGlyAsnGlnLeuLysGlyPro 100
Db	1826 AGTGATGGTCAGCATCTGGCTATTGACCTAACACAGGCAATCAGTTGAAAGGTCCA 1885
Qy	101 AspProLysArgAsnIleLysLysTyrLeu 110

Qy 101 AspProLysArgAsnIleLysLysTyrLeu 110
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